AMENDMENTS

IN THE CLAIMS

Please amend claim 37 as provided below, so that the claim set reads as follows:

1 – 36. (Canceled)

37. (Currently Amended) A method for analyzing the sequence of a template comprising:

a) capturing the template with a sequencing reagent to form a captured template, said sequencing reagent being immobilized to a solid surface and comprising:

(i) a capture moiety capable of forming a stable duplex with a region of the template nucleic acid molecule;

(ii) a primer region comprising from 3 to 7 bases; and

between said capture moiety and said primer region

(iii) a spacer region that minimizes template independent noise; and

b) scanning the captured template using a primer-polymerase complex for regions of complementarity to the primer region and forming a duplex;

c) extending the primer region by at least one nucleotide moiety by means of a template-homology dependent extension reaction to form an extended primer; and

d) detecting the extended primer, wherein said detecting of the extended primer indicates the presence of one or more regions of complementarity to the primer region in the captured template;

wherein the steps of the method are repeated for ~~an array of~~ sequencing reagents **that are bound in an array pattern onto to said solid surface** so that a pattern of signals is generated for the template.

38. (Previously presented) The method of claim 37, wherein the solid surface is glass or plastic.

39. (Previously presented) The method of claim 37, wherein the solid surface is a glass plate, a quartz wafer, a nylon membrane, a nitrocellulose membrane, or a silicon wafer.

40. (Previously presented) The method of claim 37, wherein the solid surface is silicon glass.

41. (Previously presented) The method of claim 37, wherein the solid surface is polystyrene plastic.

42. (Previously presented) The method of claim 37, wherein the sequencing reagent further comprises an attachment moiety.

43. (Previously presented) The method of claim 42, wherein the sequence reagent has a 5'-terminus and the attachment moiety is located at or near said 5'-terminus.

44. (Previously presented) The method of claim 42, wherein the attachment moiety is an amino group, a thiol group, a disulfide group, or a biotin group.

45. (Previously presented) The method of claim 37, wherein the capture moiety comprises a sequence of 8-24 cytosine bases.

46. (Previously presented) The method of claim 37, wherein the capture moiety comprises a specific sequence complementary to a PCR primer or a portion thereof.

47. (Previously presented) The method of claim 37, wherein the spacer region is at least 10 nm in length.

48. (Previously presented) The method of claim 37, wherein the spacer region comprises a random, pseudo-random, or non-random sequence of nucleotide bases or analogs thereof.

49. (Previously presented) The method of claim 37, wherein the at least one nucleotide moiety is a non-chain terminating nucleotide or an analogue of a non-chain terminating nucleotide.

50. (Previously presented) The method of claim 49, wherein the at least one nucleotide moiety is a deoxynucleoside triphosphate base or ribonucleoside triphosphate base.

51. (Previously presented) The method of claim 37, wherein the at least one nucleotide moiety is a chain terminating nucleotide analogue.

52. (Previously presented) The method of claim 51, wherein the chain terminating nucleotide analogue is a dideoxynucleotide.

53. (Previously presented) The method of claim 37, wherein the at least one nucleotide moiety has a detectable labeled.

54. (Previously presented) The method of claim 53, wherein the detectable label is a fluorescent label.

55. (Previously presented) The method of claim 53, wherein the detectable label is a radioactive isotope.

56. (Previously presented) The method of claim 53, wherein the detectable label is an electron rich molecule.

57. (Previously presented) The method of claim 37, wherein the extended primer is detected by change in mass.

58. (Previously presented) The method of claim 37, wherein the density of sequence reagents in the array is at least 1000 elements/cm^2.

59. (Previously presented) The method of claim 57, wherein said change in mass is detected through mass spectrometry.

60. (Previously presented) The method of claim 37, wherein said primer region consists of from 4 to 6 bases.

61. (Previously presented) The method of claim 37, wherein the spacer is comprised of one or more of PNA sequences, glycol groups or 5'-nitroindole groups.